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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/538,709DATE: 12/01/95
TIME: 17:15:21

INPUT SET: S7645.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Cerretti, Douglas P.

(ii) TITLE OF INVENTION: Cytokine Designated as LERK-6

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Immunex Corporation

(B) STREET: 51 University Street

(C) CITY: Seattle

(D) STATE: WA

(E) COUNTRY: USA

(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: Apple Macintosh

(C) OPERATING SYSTEM: System 7.1

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US --to be assigned--

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Malaska, Stephen L.

(B) REGISTRATION NUMBER: 32,655

(C) REFERENCE/DOCKET NUMBER: 2826

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430

(B) TELEFAX: (206) 233-0644

(2) INFORMATION FOR SEQ ID NO:1:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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47
48      (ii) MOLECULE TYPE: cDNA
49
50      (iii) HYPOTHETICAL: NO
51
52      (iv) ANTI-SENSE: NO
53
54
55      (vii) IMMEDIATE SOURCE:
56            (B) CLONE: LERK-6
57
58      (ix) FEATURE:
59            (A) NAME/KEY: CDS
60            (B) LOCATION: 1..552
61
62
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65      GCC CGG GCC AAC GCT GAC CGA TAC GCA GTC TAC TGG AAC CGT AGC AAC      48
66      Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn
67            1                    5                    10                    15
68
69      CCC AGG TTT CAG GTG AGC GCT GTG GGT GAT GGC GGC GGC TAT ACC GTG      96
70      Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Gly Tyr Thr Val
71            20                    25                    30
72
73      GAG GTG AGC ATC AAC GAC TAC CTG GAT ATC TAC TGC CCA CAC TAC GGG      144
74      Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly
75            35                    40                    45
76
77      GCG CCG CTG CCC CCG GCT GAG CGC ATG GAG CGG TAC ATC CTG TAC ATG      192
78      Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met
79            50                    55                    60
80
81      GTG AAT GGT GAG GGC CAC GCC TCC TGT GAC CAC CGG CAG CGA GGC TTC      240
82      Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe
83            65                    70                    75                    80
84
85      AAG CGC TGG GAA TGC AAC CGG CCC GCA GCG CCC GGG GGA CCC CTC AAG      288
86      Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys
87            85                    90                    95
88
89      TTC TCA GAG AAG TTC CAA CTC TTC ACC CCC TTT TCC CTG GGC TTT GAG      336
90      Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu
91            100                    105                    110
92
93      TTC CGG CCT GGC CAC GAA TAC TAC TAC ATC TCT GCC ACA CCT CCC AAC      384
94      Phe Arg Pro Gly His Glu Tyr Tyr Tyr Ile Ser Ala Thr Pro Pro Asn
95            115                    120                    125
96
97      CTC GTG GAC CGA CCC TGC CTG CGA CTC AAG GTT TAT GTG CGT CCA ACC      432
98      Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr
99            130                    135                    140
  
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100
101 AAT GAG ACC CTG TAT GAG GCT CCA GAG CCC ATC TTC ACC AGT AAC AGC      480
102 Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser
103 145                      150                      155                      160
104
105 TCC TGC AGC GGC CTG GGT GGC TGC CAC CTC TTC CTC ACC ACC GTC CCT      528
106 Ser Cys Ser Gly Leu Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro
107                      165                      170                      175
108
109 GTG CTG TGG TCC CTT CTG GGC TCC TAG      555
110 Val Leu Trp Ser Leu Leu Gly Ser
111                      180
112
113
114 (2) INFORMATION FOR SEQ ID NO:2:
115
116 (i) SEQUENCE CHARACTERISTICS:
117 (A) LENGTH: 184 amino acids
118 (B) TYPE: amino acid
119 (D) TOPOLOGY: linear
120
121 (ii) MOLECULE TYPE: protein
122
123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
124
125 Ala Arg Ala Asn Ala Asp Arg Tyr Ala Val Tyr Trp Asn Arg Ser Asn
126 1                      5                      10                      15
127
128 Pro Arg Phe Gln Val Ser Ala Val Gly Asp Gly Gly Gly Tyr Thr Val
129                20                      25                      30
130
131 Glu Val Ser Ile Asn Asp Tyr Leu Asp Ile Tyr Cys Pro His Tyr Gly
132                35                      40                      45
133
134 Ala Pro Leu Pro Pro Ala Glu Arg Met Glu Arg Tyr Ile Leu Tyr Met
135                50                      55                      60
136
137 Val Asn Gly Glu Gly His Ala Ser Cys Asp His Arg Gln Arg Gly Phe
138                65                      70                      75                      80
139
140 Lys Arg Trp Glu Cys Asn Arg Pro Ala Ala Pro Gly Gly Pro Leu Lys
141                85                      90                      95
142
143 Phe Ser Glu Lys Phe Gln Leu Phe Thr Pro Phe Ser Leu Gly Phe Glu
144                100                      105                      110
145
146 Phe Arg Pro Gly His Glu Tyr Tyr Tyr Ile Ser Ala Thr Pro Pro Asn
147                115                      120                      125
148
149 Leu Val Asp Arg Pro Cys Leu Arg Leu Lys Val Tyr Val Arg Pro Thr
150                130                      135                      140
151
152 Asn Glu Thr Leu Tyr Glu Ala Pro Glu Pro Ile Phe Thr Ser Asn Ser
    
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RAW SEQUENCE LISTING
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153 145 150 155 160
154
155 Ser Cys Ser Gly Leu Gly Gly Cys His Leu Phe Leu Thr Thr Val Pro
156 165 170 175
157
158 Val Leu Trp Ser Leu Leu Gly Ser
159 180
160

161 (2) INFORMATION FOR SEQ ID NO:3:

162

163 (i) SEQUENCE CHARACTERISTICS:

164 (A) LENGTH: 28 base pairs

165 (B) TYPE: nucleic acid

166 (C) STRANDEDNESS: single

167 (D) TOPOLOGY: linear

168

169 (ii) MOLECULE TYPE: cDNA

170

171

172

173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

174

175 GATATTTACT GCCCGCACTA CAACAGCT

28

176

177 (2) INFORMATION FOR SEQ ID NO:4:

178

179 (i) SEQUENCE CHARACTERISTICS:

180 (A) LENGTH: 25 base pairs

181 (B) TYPE: nucleic acid

182 (C) STRANDEDNESS: single

183 (D) TOPOLOGY: linear

184

185 (ii) MOLECULE TYPE: cDNA

186

187 (iii) HYPOTHETICAL: NO

188

189 (iv) ANTI-SENSE: NO

190

191

192

193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

194

195 AGAGAAGGCG CTGTAGCGCT GGAAC

25

196

197 (2) INFORMATION FOR SEQ ID NO:5:

198

199 (i) SEQUENCE CHARACTERISTICS:

200 (A) LENGTH: 31 base pairs

201 (B) TYPE: nucleic acid

202 (C) STRANDEDNESS: single

203 (D) TOPOLOGY: linear

204

205 (ii) MOLECULE TYPE: cDNA

RAW SEQUENCE LISTING
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206
207 (iii) HYPOTHETICAL: NO
208
209 (iv) ANTI-SENSE: NO
210
211
212
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
214
215 ACGTAGTCTA CTGGAAGTCC AGTAACCCCA G 31
216
217 (2) INFORMATION FOR SEQ ID NO:6:
218
219 (i) SEQUENCE CHARACTERISTICS:
220 (A) LENGTH: 34 base pairs
221 (B) TYPE: nucleic acid
222 (C) STRANDEDNESS: single
223 (D) TOPOLOGY: linear
224
225 (ii) MOLECULE TYPE: cDNA
226
227 (iii) HYPOTHETICAL: NO
228
229 (iv) ANTI-SENSE: NO
230
231
232
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
234
235 AGCCTCAAGC ACTGGCCAGA ACTCTCTCTG GAGT 34
236
237
238 (2) INFORMATION FOR SEQ ID NO:7:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 314 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: single
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: cDNA to mRNA
247
248 (iii) HYPOTHETICAL: NO
249
250 (iv) ANTI-SENSE: NO
251
252
253 (ix) FEATURE:
254 (A) NAME/KEY: CDS
255 (B) LOCATION: 2..313
256
257
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/538,709*

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Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: US --to be assigned--